

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=7; day=20; hr=11; min=59; sec=34; ms=513;]

=====

Application No:	10579290	Version No:	2.0
-----------------	----------	-------------	-----

Input Set:

Output Set:

Started:	2010-07-12 16:36:30.231
Finished:	2010-07-12 16:36:30.313
Elapsed:	0 hr(s) 0 min(s) 0 sec(s) 82 ms
Total Warnings:	0
Total Errors:	0
No. of SeqIDs Defined:	4
Actual SeqID Count:	4

SEQUENCE LISTING

<110> PATRYS PTY LIMITED

VOLLMER, Heinz

MULLER-HERMELINK, Hans-Konrad

<120> Human Monoclonal Antibody

<130> 043043-0359295

<140> 10579290

<141> 2010-07-12

<150> EP 03 026 161.4

<151> 2003-11-14

<160> 4

<170> PatentIn version 3.3

<210> 1

<211> 96

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> variable region of the light chain (VL) of antibody SAM-6

<400> 1

Ser	Tyr	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ser	Pro	Gly
1				5					10					15

Gln	Thr	Ala	Ser	Ile	Thr	Cys	Ser	Gly	Asp	Lys	Leu	Gly	Asp	Lys
				20					25					30

Tyr	Ala	Cys	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Val	Leu
				35					40					45

Val	Ile	Tyr	Gln	Asp	Ser	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg
				50					55					60

Phe	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser
				65					70					75

Gly	Thr	Gln	Ala	Met	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ala	Trp
				80					85					90

Asp Ser Ser Ile Val Val
95

<210> 2
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> variable region of the light chain (VL) of antibody SAM-6

<400> 2

tcc tat gtg ctg act cag cca ccc tca gtg tcc gtg tcc cca gga 45
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly
1 5 10 15

cag aca gcc agc atc acc tgc tct gga gat aaa ttg ggg gat aaa 90
Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys
20 25 30

tat gct tgc tgg tat cag cag aag cca ggc cag tcc cct gtg ctg 135
Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu
35 40 45

gtc atc tat caa gat agc aag cgg ccc tca ggg atc cct gag cga 180
Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
50 55 60

ttc tct ggc tcc aac tct ggg aac aca gcc act ctg acc atc agc 225
Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
65 70 75

ggg acc cag gct atg gat gag gct gac tat tac tgt cag gcg tgg 270
Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp
80 85 90

gac agc agc att gtg gta 288
Asp Ser Ser Ile Val Val
95

<210> 3
<211> 110
<212> PRT
<213> Homo sapiens

<220>

<221> misc_feature
<223> variable region of the heavy chain (VH) of antibody SAM-6

<400> 3

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly
1				5					10					15
Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser
				20					25					30
Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
				35					40					45
Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr
				50					55					60
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser
				65					70					75
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
				80					85					90
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Leu	Ala	Val	Ala	Gly
				95					100					105
Arg	Pro	Phe	Asp	Tyr										
				110										

<210> 4
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> variable region of the heavy chain (VH) of antibody SAM-6

<400> 4

cag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtg	gtc	cag	cct	ggg	45
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	
1				5					10					15	
agg	tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	agt	90
Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	
				20					25					30	

agc tat gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg 135
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gag tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac 180
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr
50 55 60

gca gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc 225
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
65 70 75

aag aac acg ctg tat ctg caa atg aac agc ctg aga gct gag gac 270
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

acg gct gtg tat tac tgt gcg aga gat cgg tta gca gtg gct ggt 315
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Ala Val Ala Gly
95 100 105

aga cct ttt gac tac 330
Arg Pro Phe Asp Tyr
110